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1	TCCCATACAGGCCCCACCATGAAGGGTTTCACAGCCACTCTCTTCTCTGGACTCTGAT	60
1	MetLysGlyPheThrAlaThrLeuPheLeuTrpThrLeuI	14
1	M K G F T A T L F L W T L I	14
61	TTTTCCAGCTGCAGTGGAGGCGGCGGTGGGAAAGCCTGGCCACACACGTGGTCTGTAG	120
15	ePheProSerCysSerGlyGlyGlyGlyGlyLysAlaTrpProThrHisValValCysSe	34
15	F P S C S G G G G G K A W P T H V V C S	34
121	CGACAGCGGCTTGAAGTGCTCTACCAGAGTTGCGATCCATTACAAGATTTGGCTTTTC	180
35	rAspSerGlyLeuGluValLeuTyrGlnSerCysAspProLeuGlnAspPheGlyPheSe	54
35	D S G L E V L Y Q S C D P L Q D F G F S	54
181	TGTTGAAAAGTGTTCCAAGCAATTAATAATCAAATATCAACATTAGATTTGGAATTATTCT	240
55	rValGluLysCysSerLysGlnLeuLysSerAsnIleAsnIleArgPheGlyIleIleLe	74
55	V E K C S K Q L K S N I N I R F G I I L	74
241	GAGAGAGGACATCAAAGAGCTTTTTCTTGACCTAGCTCTCATGTCTCAAGGCTCATCTGT	300
75	uArgGluAspIleLysGluLeuPheLeuAspLeuAlaLeuMetSerGlnGlySerSerVa	94
75	R E D I K E L F L D L A L M S Q G S S V	94
301	TTTGAATTTCTCCTATCCCATCTGTGAGGCGGCTCTGCCAAGTTTTCTTTCTGTGGAAG	360
95	lLeuAsnPheSerTyrProIleCysGluAlaAlaLeuProLysPheSerPheCysGlyAr	114
95	L N F S Y P I C E A A L P K F S F C G R	114
361	AAGGAAAGGAGAGCAGATTTACTATGCTGGGCTGTCAATAATCCTGAATTTACTATTCC	420
115	gArgLysGlyGluGlnIleTyrTyrAlaGlyProValAsnAsnProGluPheThrIlePr	134
115	R K G E Q I Y Y A G P V N N P E F T I P	134
421	TCAGGGAGAATACCAGGTTTTGCTGGAACGTACACTGAAAAACGGTCCACCGTGGCCTG	480
135	oGlnGlyGluTyrGlnValLeuLeuGluLeuTyrThrGluLysArgSerThrValAlaCy	154
135	Q G E Y Q V L L E L Y T E K R S T V A C	154
481	TGCCAATGCTACTATCATGTGCTCCTGACTGTGGCCTGTAGCAAAAATCAGCCAGCTG	540
155	sAlaAsnAlaThrIleMetCysSerEnd	162
155	A N A T I M C S *	162
541	CATCTCGTGGGACCTCCAAGCTCCTCTGACTGAACCTACTGTGGGAGGAGAAGCAGCTGA	600
541		600

FIG. 1A

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601      TGACAGAGAGAGGCTCTACAAAGAAGCGCCCCCAAAGAGTGCAGCTGCTAATTTTAGTCC      660
      -----+-----+-----+-----+-----+-----+-----+
661      CAGGACCAGACATCCCCAGACTCCACAGATGTAATGAAGTCCCGAATGTA1CTGTTTCT      720
      -----+-----+-----+-----+-----+-----+-----+
721      AAGGAGCCTCTTGGCAGTCCTTAAGCAGTCTTGAGGGTCCATCCTTTTTCTCTAATTGGT      780
      -----+-----+-----+-----+-----+-----+-----+
781      CGCCTCCCACCAGACTCACCTGCTTTTCAACTTTT2AGGAGTGCTTCCTCACAGTTACCA      840
      -----+-----+-----+-----+-----+-----+-----+
841      AGAAATAAAGAAAGCTGGCC      860
      -----+-----+-----+-----+-----+-----+-----+
```

Nucleotide sequence of Human MD-1 Homolog. Corresponding deduced amino-acid sequence shown below using standard three and one letter abbreviation.

FIG.1B

106020 260000

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Score = 344 (160.0 bits), Expect = 6.6e-44, P = 6.6e-44
 Identities = 60/133 (45%), Positives = 86/133 (64%)

```

Query:   27 WPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKSNINIRFGIILREDIKELFLDLA  86
          WPTH VC +  LE+ Y+SCDP QDF FS+++CS      +IR ++LR+ IKEL+  +
Sbjct:   22 WPTH TVCKEENLEIYYKSCDPQQDFAFSIDRCSDVTTHTFDIRAAMVLRQSIKELYAKVD  81

Query:   87 LMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQIYYAGPVNNPEFTIPQGEYQVLLKLYT  146
          L+  G +VL++S  +C  L K  FCG++KGE +YY GP+      IPQG+Y +  L
Sbjct:   62 LIINGKTVLSYSETLCGPGLSKLIFCGKKKGEHLYYEGPITLGIKEIPQGDYTITARLTN  141

Query:   147 EKRSTVACANATI  159
          E R+TVACA+ T+
Sbjct:   142 EDRATVACADFTV  154
  
```

Sequence comparison between human MD-1 protein (upper line) and MD-1 protein from chicken (lower line).

FIG.2

1488.0440003 EKS/PSC

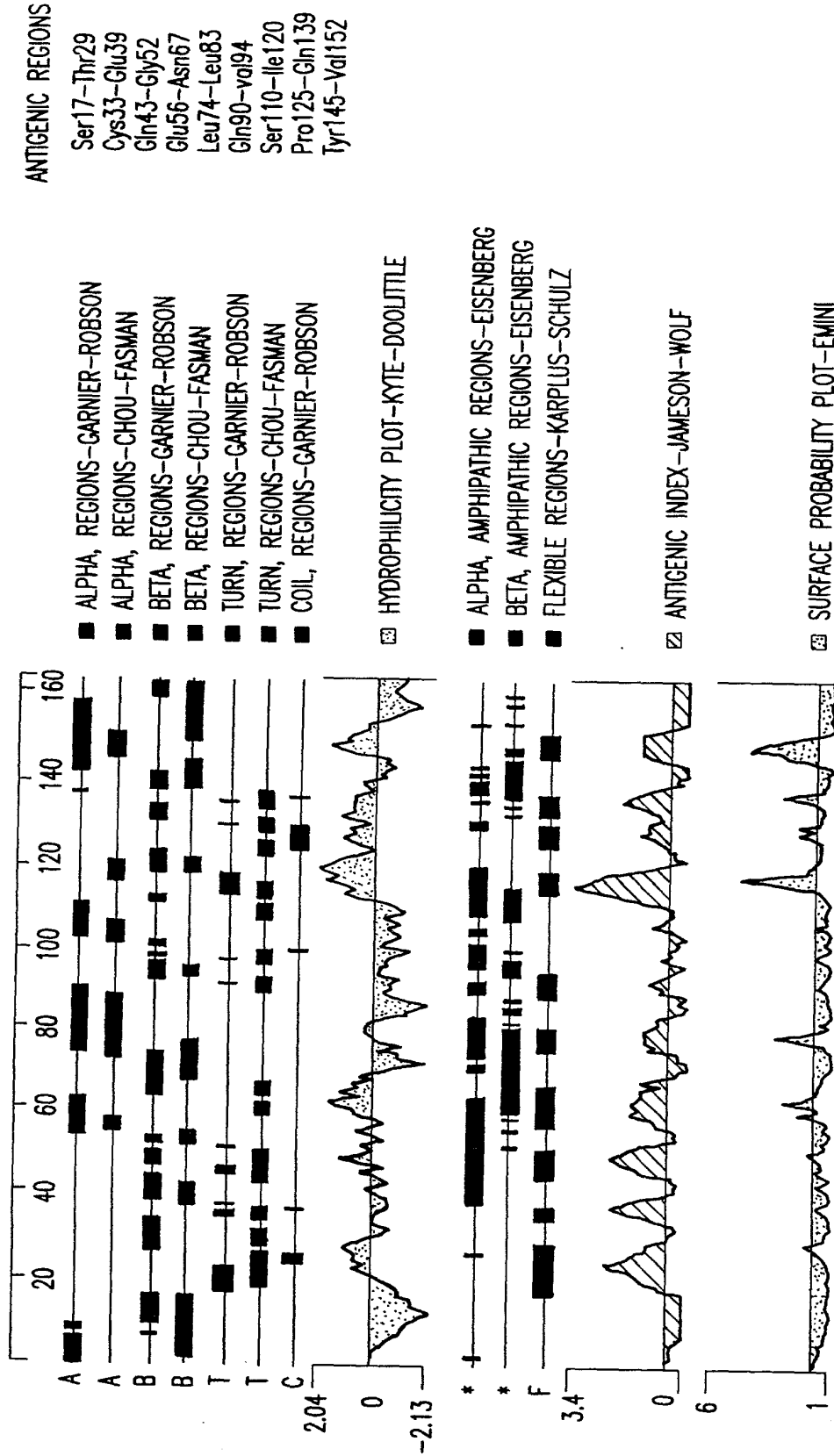


FIG.3

Letter to the Editor

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Query:      27 WPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQKSNINIRPGTILREDIKELFLDLA 86
            WPTH VC + LE+ Y+SCDP QDF FS+++CS      +IR ++LR+ IKEL+ +
Sbjct:      22 WPTHVCKEENLELYYKSCDPQDFAFSIDRCSQVTTHTFDIRAMVLRQSDIKELYAKVD 81

Query:      87 LMSQGGSSVLNFSYPICEAALPKFSEFCGRKGEQIYYAGPVNNPEFTIPQGEYQVIAJHYT 146
            L+  G +VL++S +C  L K FCG++KGE +YY GP+  IPQG+Y +  L
Sbjct:      82 LILNGATVLSYSEILCGPGLSKLDFCGKKKGHEHLYYEGPITLGIKEH+QGQVTTTARLN 141

Query:      147 EKRSTVACANATI 159
            E R+TVACA+ T+
Sbjct:      142 EDRAIVACADFV 154

```

Figure 2. Sequence comparison between human MD-1 protein (upper line) and MD-1 protein from chicken (lower line).

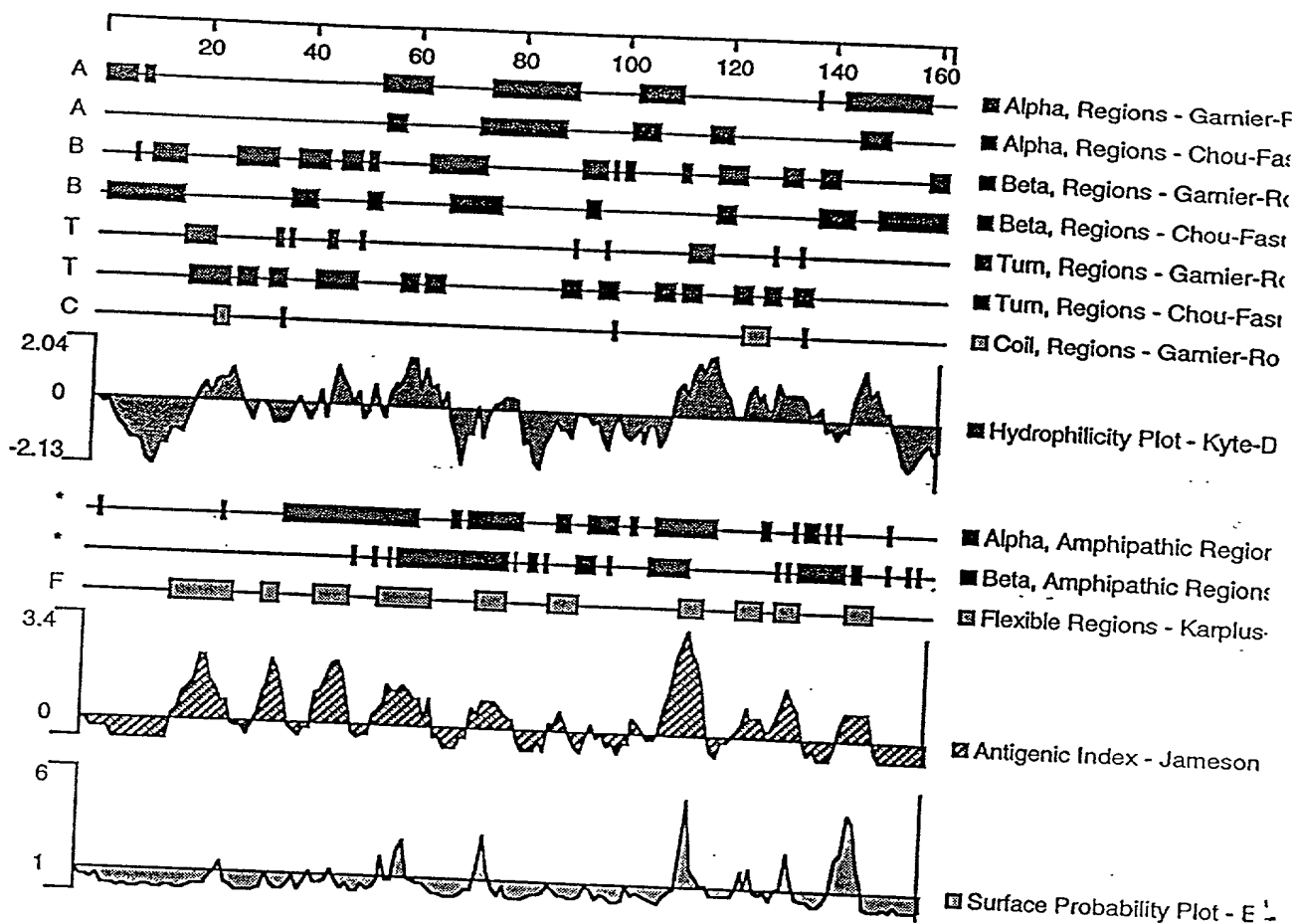


Figure 3. Analysis of the full length predicted amino acid sequence.

Antigenic regions

Ser17- Thr29
 Cys33-Glu39
 Gln43-Gly52
 Glu56-Asn67
 Leu74-Leu83
 Gln90-val94
 Ser110-Ile120
 Pro125-Gln139
 Tyr145-Val152